

10/797,262
SEQUENCE LISTING

<110> East Tennessee State University Research Foundation
Lampson, Bert
Velore, Jashree

<120> RNA-DEPENDENT DNA POLYMERASE FROM GEOBACILLUS STEAROTHERMOPHILUS

<130> 2826067.000002

<140> 10/797,262

<141> 2004-03-10

<160> 18

<170> PatentIn version 3.5

<210> 1

<211> 1263

<212> DNA

<213> Geobacillus stearothermophilus

<220>

<221> CDS

<222> (1)..(1263)

<400> 1
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1 5 10 15
ctc aaa cgg gtc gaa gcc aac caa gga gca ccg gga atc gac gga gta 96
Leu Lys Arg Val Glu Ala Asn Gln Gly Ala Pro Gly Ile Asp Gly Val
20 25 30
tca acc gat caa ctc cgt gat tac atc cgc gct cac tgg agc acg atc 144
Ser Thr Asp Gln Leu Arg Asp Tyr Ile Arg Ala His Trp Ser Thr Ile
35 40 45
cgc gcc caa ctc ttg gcg gga acc tac ccg ccg gcg cct gtc cgc agg 192
Arg Ala Gln Leu Leu Ala Gly Thr Tyr Arg Pro Ala Pro Val Arg Arg
50 55 60
gtc gga atc ccg aaa ccg ggc ggc ggc aca ccg cag cta ggc att ccc 240
Val Gly Ile Pro Lys Pro Gly Gly Gly Thr Arg Gln Leu Gly Ile Pro
65 70 75 80
acc gtg gtg gac cgg ctg atc caa caa gcc att ctt caa gaa ctc aca 288
Thr Val Val Asp Arg Leu Ile Gln Ala Ile Leu Gln Glu Leu Thr
85 90 95
ccc att ttc gat cca gac ttc tcc cct tcc agc ttc gga ttc cgt ccg 336
Pro Ile Phe Asp Pro Asp Phe Ser Pro Ser Ser Phe Gly Phe Arg Pro
100 105 110
ggc cgt aac gcc cac gat gcc gtg ccg caa gcg caa ggc tac atc cag 384
Gly Arg Asn Ala His Asp Ala Val Arg Gln Ala Gln Gly Tyr Ile Gln
115 120 125
gaa ggg tat cgg tac gtg gtc gac atg gac ctg gaa aag ttc ttt gat 432
Glu Gly Tyr Arg Tyr Val Val Asp Met Asp Leu Glu Lys Phe Phe Asp
130 135 140

1 Replacement Sheet

cgg gtc aac cat gac atc ttg atg agt cgg gtg gcc cga aaa gtc aag Arg Val Asn His Asp Ile Leu Met Ser Arg Val Ala Arg Lys Val Lys 145 150 155 160	480
gat aaa cgc gtg ctg aaa ctg atc cgt gcc tac ctg caa gcc ggc gtt Asp Lys Arg Val Leu Lys Ile Arg Ala Tyr Leu Gln Ala Gly Val 165 170 175	528
atg atc gaa ggg gtg aag gtg cag acg gag gaa ggg acg ccg caa ggc Met Ile Glu Gly Val Lys Val Gln Thr Glu Gly Thr Pro Gln Gly 180 185 190	576
ggc ccc ctc agc ccc ctg ctg gcg aac atc ctt ctc gac gat tta gac Gly Pro Leu Ser Pro Leu Leu Ala Asn Ile Leu Leu Asp Asp Leu Asp 195 200 205	624
aag gaa ttg gag aag cga gga ttg aaa ttc tgc cgt tac gca gat gac Lys Glu Leu Glu Lys Arg Gln Lys Phe Cys Arg Tyr Ala Asp Asp 210 215 220	672
tgc aac atc tat gtg aaa agt ctg cgg gca gga caa cgg gtg aaa caa Cys Asn Ile Tyr Val Lys Ser Leu Arg Ala Gly Gln Arg Val Lys Gln 225 230 235 240	720
agc atc caa cgg ttc ttg gag aaa acg ctc aaa ctc aaa gta aac gag Ser Ile Gln Arg Phe Leu Glu Lys Thr Leu Lys Leu Lys Val Asn Glu 245 250 255	768
gag aaa agt gcg gtg gac cgc ccg tgg aaa cgg gcc ttt ctg ggg ttt Glu Lys Ser Ala Val Asp Arg Pro Trp Lys Arg Ala Phe Leu Gly Phe 260 265 270	816
agc ttc aca ccg gaa cga aaa gcg cga atc cgg ctc gcc cca agg tcg Ser Phe Thr Pro Glu Arg Lys Ala Arg Ile Arg Leu Thr Ala Pro Arg Ser 275 280 285	864
att caa cgt ctg aaa cag cgg att cga cag ctg acc aac cca aac tgg Ile Gln Arg Leu Lys Gln Arg Ile Arg Gln Leu Thr Asn Pro Asn Trp 290 295 300	912
agc ata tcg atg cca gaa cga att cat cgc gtc aat caa tac gtc atg Ser Ile Ser Met Pro Glu Arg Ile His Arg Val Asn Gln Tyr Val Met 305 310 315 320	960
gga tgg atc ggg tat ttt cgg ctc gtc gaa acc ccg tct gtc ctt cag Gly Trp Ile Gly Tyr Phe Arg Leu Val Glu Thr Gln Pro Ser Val Leu Gln 325 330 335	1008
acc atc gaa gga tgg att cgg agg agg ctt cga ctc tgt caa tgg ctt Thr Ile Glu Gly Trp Ile Arg Arg Arg Leu Arg Leu Cys Gln Trp Leu 340 345 350	1056
caa tgg aaa cgg gtc aga acc aga atc cgt gag tta aga gcg ctg ggg Gln Trp Lys Arg Val Arg Thr Arg Ile Arg Glu Leu Arg Ala Leu Gly 355 360 365	1104
ctg aaa gag aca gcg gtg atg gag atc gcc aat acc cga aaa gga gct Leu Lys Glu Thr Ala Val Met Glu Ile Ala Asn Thr Arg Lys Gly Ala 370 375 380	1152
tgg cga aca acg aaa acg ccg caa ctc cac cag gcc ctg ggc aaa acc Trp Arg Thr Thr Lys Thr Pro Gln Leu His Gln Ala Leu Gly Lys Thr 385 390 395	1200

385					390					10/797,262					400	
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	Tyr	Trp	Thr	Ala	Gln	Gly	Leu	Lys	Ser	Leu	Thr	Gln	Arg	Tyr	Phe	Glu
					405					410					415	
	ctc	cg	caa	gg	tga											
	Leu	Arg	Gln	Gly												
				420												
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	Leu	Lys	Arg	Val	Glu	Ala	Asn	Gln	Gly	Ala	Pro	Gly	Ile	Asp	Gly	Val
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	Ser	Thr	Asp	Gln	Leu	Arg	Asp	Tyr	Ile	Arg	Ala	His	Trp	Ser	Thr	Ile
			35					40					45			
	Arg	Ala	Gln	Leu	Leu	Ala	Gly	Thr	Tyr	Arg	Pro	Ala	Pro	Val	Arg	Arg
		50					55					60				
	Val	Gly	Ile	Pro	Lys	Pro	Gly	Gly	Gly	Thr	Arg	Gln	Leu	Gly	Ile	Pro
	65					70					75				80	
	Thr	Val	Val	Asp	Arg	Leu	Ile	Gln	Gln	Ala	Ile	Leu	Gln	Glu	Leu	Thr
					85					90					95	
	Pro	Ile	Phe	Asp	Pro	Asp	Phe	Ser	Pro	Ser	Ser	Phe	Gly	Phe	Arg	Pro
				100					105					110		
	Gly	Arg	Asn	Ala	His	Asp	Ala	Val	Arg	Gln	Ala	Gln	Gly	Tyr	Ile	Gln
			115					120					125			
	Glu	Gly	Tyr	Arg	Tyr	Val	Val	Asp	Met	Asp	Leu	Glu	Lys	Phe	Phe	Asp
		130					135					140				
	Arg	Val	Asn	His	Asp	Ile	Leu	Met	Ser	Arg	Val	Ala	Arg	Lys	Val	Lys
	145					150					155					160
	Asp	Lys	Arg	Val	Leu	Lys	Leu	Ile	Arg	Ala	Tyr	Leu	Gln	Ala	Gly	Val
					165					170					175	
	Met	Ile	Glu	Gly	Val	Lys	Val	Gln	Thr	Glu	Glu	Gly	Thr	Pro	Gln	Gly
									3							

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180	185	190
Gly Pro Leu Ser Pro Leu Leu Ala Asn Ile Leu Leu Asp Asp Leu Asp 195 200 205		
Lys Glu Leu Glu Lys Arg Gly Leu Lys Phe Cys Arg Tyr Ala Asp Asp 210 215 220		
Cys Asn Ile Tyr Val Lys Ser Leu Arg Ala Gly Gln Arg Val Lys Gln 225 230 235 240		
Ser Ile Gln Arg Phe Leu Glu Lys Thr Leu Lys Leu Lys Val Asn Glu 245 250 255		
Glu Lys Ser Ala Val Asp Arg Pro Trp Lys Arg Ala Phe Leu Gly Phe 260 265 270		
Ser Phe Thr Pro Glu Arg Lys Ala Arg Ile Arg Leu Ala Pro Arg Ser 275 280 285		
Ile Gln Arg Leu Lys Gln Arg Ile Arg Gln Leu Thr Asn Pro Asn Trp 290 295 300		
Ser Ile Ser Met Pro Glu Arg Ile His Arg Val Asn Gln Tyr Val Met 305 310 315 320		
Gly Trp Ile Gly Tyr Phe Arg Leu Val Glu Thr Pro Ser Val Leu Gln 325 330 335		
Thr Ile Glu Gly Trp Ile Arg Arg Arg Leu Arg Leu Cys Gln Trp Leu 340 345 350		
Gln Trp Lys Arg Val Arg Thr Arg Ile Arg Glu Leu Arg Ala Leu Gly 355 360 365		
Leu Lys Glu Thr Ala Val Met Glu Ile Ala Asn Thr Arg Lys Gly Ala 370 375 380		
Trp Arg Thr Thr Lys Thr Pro Gln Leu His Gln Ala Leu Gly Lys Thr 385 390 395 400		
Tyr Trp Thr Ala Gln Gly Leu Lys Ser Leu Thr Gln Arg Tyr Phe Glu 405 410 415		
Leu Arg Gln Gly 420		

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<210> 3
 <211> 420
 <212> PRT
 <213> *Geobacillus stearothermophilus*

<220>
 <221> PEPTIDE
 <222> (1)..(420)

<400> 3

Met Ala Leu Leu Glu Arg Ile Leu Ala Arg Asp Asn Leu Ile Thr Ala
 1 5 10 15

Leu Lys Arg Val Glu Ala Asn Gln Gly Ala Pro Gly Ile Asp Gly Val
 20 25 30

Ser Thr Asp Gln Leu Arg Asp Tyr Ile Arg Ala His Trp Ser Thr Ile
 35 40 45

Arg Ala Gln Leu Leu Ala Gly Thr Tyr Arg Pro Ala Pro Val Arg Arg
 50 55 60

Val Gly Ile Pro Lys Pro Gly Gly Gly Thr Arg Gln Leu Gly Ile Pro
 65 70 75 80

Thr Val Val Asp Arg Leu Ile Gln Gln Ala Ile Leu Gln Glu Leu Thr
 85 90 95

Pro Ile Phe Asp Pro Asp Phe Ser Pro Ser Ser Phe Gly Phe Arg Pro
 100 105 110

Gly Arg Asn Ala His Asp Ala Val Arg Gln Ala Gln Gly Tyr Ile Gln
 115 120 125

Glu Gly Tyr Arg Tyr Val Val Asp Met Asp Leu Glu Lys Phe Phe Asp
 130 135 140

Arg Val Asn His Asp Ile Leu Met Ser Arg Val Ala Arg Lys Val Lys
 145 150 155 160

Asp Lys Arg Val Leu Lys Leu Ile Arg Ala Tyr Leu Gln Ala Gly Val
 165 170 175

Met Ile Glu Gly Val Lys Val Gln Thr Glu Glu Gly Thr Pro Gln Gly
 180 185 190

Gly Pro Leu Ser Pro Leu Leu Ala Asn Ile Leu Leu Asp Asp Leu Asp
 195 200 205

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Lys Glu Leu Glu Lys Arg Gly Leu Lys Phe Cys Arg Tyr Ala Asp Asp
210 215 220

Cys Asn Ile Tyr Val Lys Ser Leu Arg Ala Gly Gln Arg Val Lys Gln
225 230 235 240

Ser Ile Gln Arg Phe Leu Glu Lys Thr Leu Lys Leu Lys Val Asn Glu
245 250 255

Glu Lys Ser Ala Val Asp Arg Pro Trp Lys Arg Ala Phe Leu Gly Phe
260 265 270

Ser Phe Thr Pro Glu Arg Lys Ala Arg Ile Arg Leu Ala Pro Arg Ser
275 280 285

Ile Gln Arg Leu Lys Gln Arg Ile Arg Gln Leu Thr Asn Pro Asn Trp
290 295 300

Ser Ile Ser Met Pro Glu Arg Ile His Arg Val Asn Gln Tyr Val Met
305 310 315 320

Gly Trp Ile Gly Tyr Phe Arg Leu Val Glu Thr Pro Ser Val Leu Gln
325 330 335

Thr Ile Glu Gly Trp Ile Arg Arg Arg Leu Arg Leu Cys Gln Trp Leu
340 345 350

Gln Trp Lys Arg Val Arg Thr Arg Ile Arg Glu Leu Arg Ala Leu Gly
355 360 365

Leu Lys Glu Thr Ala Val Met Glu Ile Ala Asn Thr Arg Lys Gly Ala
370 375 380

Trp Arg Thr Thr Lys Thr Pro Gln Leu His Gln Ala Leu Gly Lys Thr
385 390 395 400

Tyr Trp Thr Ala Gln Gly Leu Lys Ser Leu Thr Gln Arg Tyr Phe Glu
405 410 415

Leu Arg Gln Gly
420

<210> 4
<211> 1370
<212> DNA
<213> Artificial

<220>

<223> Plasmid construct

<220>

<221> misc_feature

<222> (1)..(1370)

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atatgcggca agacctgaat ctcatccgc ggaaggagaa gatcacgatg gctttgttgg	120
aacgcatctt agcgagagac aacctcatca cggcgctcaa acgggtcgaa gccaaccaag	180
gagcaccggg aatcgacgga gtatcaaccg atcaactccg tgattacatc cgcgctcact	240
ggagcacgat ccgcgcccac ctcttggcgg gaacctaccg gccggcgccct gtccgcaggg	300
tcggaatccc gaaaccgggc gccggcacac ggacgctagg cattcccacc gtggtggaac	360
ggctgatcca acaagccatt ctcaagaac tcacaccat ttctgatcca gacttctccc	420
cttcagctt cggattccgt cggggccgta acgcccacga tgcggtgcgg caagcgcaag	480
gctacatcca ggaagggtat cggtagctgg tcgacatgga cctggaaaag ttctttgatc	540
gggtcaacca tgacatcttg atgagtcggg tggcccgaaa agtcaaggat aaacgcgtgc	600
tgaactgat ccgtgacctac ctgcaagcgg gcgttatgat cgaaggggtg aaggtgcaga	660
cggaggaagg gacgcgcgaa gccggccccc tcagcccctt gctggcgaaac atccttctcg	720
acgatttaga caaggaattg gagaagcgag gattgaaatt ctgccgttac gcagatgact	780
gcaacatcta tgtgaaaagt ctgcgggcag gacaacgggt gaaacaaagc atccaacggt	840
tcttgaggaa aacgctcaaa ctcaaagtaa acgaggagaa aagtgcgggtg gaccgccgt	900
ggaacggggc ctttctgggg tttagcttca caccggaacg aaaagcgcgga atccggctcg	960
ccccaaagtc gattcaacgt ctgaaacagc ggattcgaca gctgaccaac ccaaactgga	1020
gcatactgat gccagaacga attcatcgcg tcaatcaata cgtcatggga tggatcgggt	1080
attttcggct cgtcgaaacc ccgtctgtcc ttcagaccat cgaaggatgg attcggagga	1140
ggcttcgact ctgtcaatgg ctccaatgga aacgggtcag aaccagaatc cgtgagttaa	1200
gagcgctggg gctgaaagag acagcggtag tggagatcgc caataccgga aaaggagctt	1260
ggcgaacaac gaaaacgcgg caactccacc aggcctctgg caaaacctac tggaccgcct	1320
aagggtctca gagtttgacg caacgatatt tcgaactccg tcaaggttga	1370

<210> 5

<211> 32

<212> DNA

<213> Artificial

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<223> Nucleotide primer containing NdeI restriction site

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 agacaacata tgcggcaaga cctgaatctc at 32

<210> 6
 <211> 28
 <212> DNA
 <213> Artificial
 <220>
 <223> Nucleotide primer containing BamHI restriction site
 <400> 6
 aatggatccg ctggcgaaga tccttctc 28

<210> 7
 <211> 29
 <212> DNA
 <213> Artificial
 <220>
 <223> Nucleotide primer containing PstI restriction site
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 <221> primer_bind
 <222> (1)..(29)
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 attactgcag agcgggtccag taggttttg 29

<210> 8
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 <212> DNA
 <213> Artificial
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 <223> Nucleotide primer containing HindIII restriction site
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 <221> primer_bind
 <222> (1)..(31)
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 actcaagctt gagaagggtc tgacgttcac g 31

<210> 9
 <211> 455
 <212> PRT
 <213> Artificial
 <220>
 <223> Amino acid sequence of fusion protein

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<220>
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<222> (1)..(455)

<220>
<221> PEPTIDE
<222> (1)..(455)

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Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro
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Arg Gly Ser His Met Arg Gln Asp Leu Asn Leu Ile Pro Arg Lys Glu
20 25 30

Lys Ile Thr Met Ala Leu Leu Glu Arg Ile Leu Ala Arg Asp Asn Leu
35 40 45

Ile Thr Ala Leu Lys Arg Val Glu Ala Asn Gln Gly Ala Pro Gly Ile
50 55 60

Asp Gly Val Ser Thr Asp Gln Leu Arg Asp Tyr Ile Arg Ala His Trp
65 70 75 80

Ser Thr Ile Arg Ala Gln Leu Leu Ala Gly Thr Tyr Arg Pro Ala Pro
85 90 95

Val Arg Arg Val Gly Ile Pro Lys Pro Gly Gly Gly Thr Arg Gln Leu
100 105 110

Gly Ile Pro Thr Val Val Asp Arg Leu Ile Gln Gln Ala Ile Leu Gln
115 120 125

Glu Leu Thr Pro Ile Phe Asp Pro Asp Phe Ser Pro Ser Ser Phe Gly
130 135 140

Phe Arg Pro Gly Arg Asn Ala His Asp Ala Val Arg Gln Ala Gln Gly
145 150 155 160

Tyr Ile Gln Glu Gly Tyr Arg Tyr Val Val Asp Met Asp Leu Glu Lys
165 170 175

Phe Phe Asp Arg Val Asn His Asp Ile Leu Met Ser Arg Val Ala Arg
180 185 190

Lys Val Lys Asp Lys Arg Val Leu Lys Leu Ile Arg Ala Tyr Leu Gln
195 200 205

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 Ala Gly Val Met Ile Glu Gly Val Lys Val Gln Thr Glu Glu Gly Thr
 210 215 220
 Pro Gln Gly Gly Pro Leu Ser Pro Leu Leu Ala Asn Ile Leu Leu Asp
 225 230 235
 Asp Leu Asp Lys Glu Leu Glu Lys Arg Gly Leu Lys Phe Cys Arg Tyr
 245 250 255
 Ala Asp Asp Cys Asn Ile Tyr Val Lys Ser Leu Arg Ala Gly Gln Arg
 260 265 270
 Val Lys Gln Ser Ile Gln Arg Phe Leu Glu Lys Thr Leu Lys Leu Lys
 275 280 285
 Val Asn Glu Glu Lys Ser Ala Val Asp Arg Pro Trp Lys Arg Ala Phe
 290 295 300
 Leu Gly Phe Ser Phe Thr Pro Glu Arg Lys Ala Arg Ile Arg Leu Ala
 305 310 315
 Pro Arg Ser Ile Gln Arg Leu Lys Gln Arg Ile Arg Gln Leu Thr Asn
 325 330 335
 Pro Asn Trp Ser Ile Ser Met Pro Glu Arg Ile His Arg Val Asn Gln
 340 345 350
 Tyr Val Met Gly Trp Ile Gly Tyr Phe Arg Leu Val Glu Thr Pro Ser
 355 360 365
 Val Leu Gln Thr Ile Glu Gly Trp Ile Arg Arg Arg Leu Arg Leu Cys
 370 375 380
 Gln Trp Leu Gln Trp Lys Arg Val Arg Thr Arg Ile Arg Glu Leu Arg
 385 390 395 400
 Ala Leu Gly Leu Lys Glu Thr Ala Val Met Glu Ile Ala Asn Thr Arg
 405 410 415
 Lys Gly Ala Trp Arg Thr Thr Lys Thr Pro Gln Leu His Gln Ala Leu
 420 425 430
 Gly Lys Thr Tyr Trp Thr Ala Gln Gly Leu Lys Ser Leu Thr Gln Arg
 435 440 445
 Tyr Phe Glu Leu Arg Gln Gly
 450 455

<210> 10
 <211> 25
 <212> DNA
 <213> Artificial
 <220>
 <223> Primer sequence
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 <221> prim_transcript
 <222> (1)..(25)
 <400> 10
 cgtgggtgac acgcagacct cttac 25
 <210> 11
 <211> 25
 <212> DNA
 <213> Artificial
 <220>
 <223> Primer sequence
 <220>
 <221> prim_transcript
 <222> (1)..(25)
 <400> 11
 tcaacactgt acggcaccgc cattc 25
 <210> 12
 <211> 24
 <212> DNA
 <213> Artificial
 <220>
 <223> Primer sequence
 <220>
 <221> prim_transcript
 <222> (1)..(24)
 <400> 12
 ggtctctttt agagatttac agtg 24
 <210> 13
 <211> 394
 <212> PRT
 <213> Bacillus halodurans
 <220>
 <221> PEPTIDE
 <222> (1)..(394)
 <400> 13

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Met Leu Glu Arg Ile Leu Ser Arg Glu Asn Leu Ile Gln Leu Glu Arg
1 5 10 15

Val Glu Lys Asn Lys Gly Ser Tyr Gly Val Asp Glu Met Asp Val Lys
20 25 30

Ser Leu Arg Leu His Leu His Glu Asn Trp Thr Ser Ile Arg Asn Glu
35 40 45

Ile Ile Glu Gly Ser Tyr Phe Pro Lys Pro Val Arg Arg Val Glu Ile
50 55 60

Pro Lys Pro Asn Gly Gly Val Arg Lys Leu Gly Ile Pro Thr Val Met
65 70 75 80

Asp Arg Phe Leu Gln Gln Ala Ile Ala Gln Ile Leu Thr Gln Leu Tyr
85 90 95

Asp Pro Thr Phe Ser Glu Arg Ser Phe Gly Phe Arg Pro His Arg Arg
100 105 110

Gly His Asn Ala Val Arg Gln Ala Lys Gln Trp Met Lys Glu Gly Tyr
115 120 125

Arg Trp Val Val Asp Ile Asp Leu Glu Lys Phe Phe Asp Lys Val Asn
130 135 140

His Asp Arg Leu Met Arg Lys Leu Ser Ser Arg Ile Gln Asp Pro Arg
145 150 155 160

Val Leu Gly Leu Ile Arg Arg Tyr Leu Gln Thr Gly Val Met Glu Arg
165 170 175

Gly Leu Val Ser Pro Asn Thr Glu Gly Thr Pro Gln Gly Gly Pro Leu
180 185 190

Ser Pro Leu Leu Ser Asn Ile Val Leu Asp Glu Leu Asp Asn Glu Leu
195 200 205

Glu Lys Arg Gly Leu Lys Phe Val Arg Tyr Ala Asp Asp Cys Asn Ile
210 215 220

Tyr Val Arg Ser Lys Arg Ala Gly Leu Arg Ile Met Glu Ser Val Thr
225 230 235 240

Ser Phe Ile Glu Asn Arg Leu Lys Leu Lys Val Asn Arg Glu Lys Ser
245 250 255

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Ala Val Asp Arg Pro Trp Asn Arg Lys Phe Leu Gly Phe Ser Phe Thr
260 265 270

Arg Gly Lys Asp Pro Lys Met Arg Val Ser Lys Glu Ser Val Lys Arg
275 280 285

Leu Lys Gln Arg Ile Arg Glu Leu Thr Ser Arg Arg His Ser Met Lys
290 295 300

Met Ser Asp Arg Leu Arg Arg Leu Asn Arg Tyr Leu Thr Gly Trp Leu
305 310 315 320

Gly Tyr Tyr Gln Val Val Asp Thr Pro Ser Ile Leu Ala Gln Ile Asp
325 330 335

Ala Trp Ile Arg Arg Arg Leu Arg Met Ile Arg Trp Lys Glu Trp Lys
340 345 350

Thr Thr Ser Ala Arg Gln Lys Asn Leu Val Arg Leu Gly Ile Lys Lys
355 360 365

Ala Lys Ala Trp Gln Trp Ala Asn Ser Arg Lys Gly Tyr Trp Arg Val
370 375 380

Ala His Ser Pro Ile Met Asp Tyr Ala Leu
385 390

<210> 14
<211> 449
<212> PRT
<213> Clostridium acetobutylicum

<220>
<221> PEPTIDE
<222> (1)..(449)

<400> 14

Met Lys Asn Ser Lys Glu Met Gln Lys Leu Gln Thr Thr Ser Tyr Lys
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Glu Gly Trp Ser Cys Glu Ile Arg Val Glu Leu Gln Asn Ser Thr Arg
20 25 30

Ala His Ser Ile Ser Thr Ala Phe Asp Arg Arg Lys Asp Asp Gly Lys
35 40 45

Leu Tyr Glu Thr Asn Leu Leu Glu Arg Ile Leu Asp Arg Gln Asn Met
13 Replacement Sheet

50

55

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60

Asn Leu Ala Tyr Lys Arg Val Lys Ser Asn Lys Gly Ser His Gly Val
 65 70 80
 Asp Gly Met Lys Val Asp Glu Leu Leu Gln Tyr Leu Lys Gln Asn Gly
 85 90 95
 Lys Thr Leu Ile Ala Ser Ile Phe Asn Gly Lys Tyr Cys Pro Lys Ala
 100 105 110
 Val Arg Arg Val Glu Ile Pro Lys Pro Asp Gly Gly Ile Arg Leu Leu
 115 120 125
 Gly Ile Pro Thr Val Val Asp Arg Thr Ile Gln Gln Ala Ile Ser Gln
 130 135 140
 Val Leu Thr Pro Ile Phe Glu Lys Thr Phe Ser Glu Asn Ser Tyr Gly
 145 150 155 160
 Phe Arg Pro Lys Arg Ser Ala Lys Gln Ala Ile Lys Lys Ala Lys Glu
 165 170 175
 Tyr Met Glu Glu Gly Tyr Lys Trp Val Val Asp Ile Asp Leu Ala Lys
 180 185 190
 Tyr Phe Asp Thr Val Asn His Asp Lys Leu Met Ala Leu Val Ala Arg
 195 200 205
 Lys Ile Lys Asp Lys Arg Val Leu Lys Leu Ile Arg Leu Tyr Leu Gln
 210 215 220
 Ser Gly Val Met Ile Asn Gly Val Val Ser Glu Thr Glu Arg Gly Cys
 225 230 235 240
 Pro Gln Gly Gly Pro Leu Ser Pro Leu Leu Ser Asn Ile Met Leu Thr
 245 250 255
 Glu Leu Asp Arg Glu Leu Glu Lys Arg Gly His Lys Phe Cys Arg Tyr
 260 265 270
 Ala Asp Asp Asn Asn Val Tyr Val Arg Ser Lys Lys Ala Gly Asp Arg
 275 280 285
 Val Met Arg Ser Ile Thr Arg Phe Ile Glu Asn Lys Leu Lys Leu Lys
 290 295 300

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Val Asn Lys Glu Lys Ser Ala Val Asp Arg Pro Trp Arg Arg Lys Phe
305 310 315 320

Leu Gly Phe Thr Phe Tyr Gln Trp Tyr Gly Lys Ile Gly Ile Arg Val
325 330 335

His Glu Lys Ser Val Lys Lys Phe Lys Ala Lys Ile Lys Ala Ile Thr
340 345 350

Ala Arg Ser Asn Ala Leu Asn Ile Glu Asn Arg Ile Ile Lys Leu Arg
355 360 365

Gln Cys Ile Ile Gly Trp Leu Asn Tyr Phe Gly Ile Ala Glu Met Thr
370 375 380

Lys Leu Ala Lys Lys Leu Asp Glu Trp Thr Arg Arg Arg Leu Arg Met
385 390 395 400

Cys Tyr Trp Lys Gln Trp Lys Lys Val Lys Thr Lys Tyr Asp Asn Leu
405 410 415

Arg Lys Phe Gly Ile Asn Asn Ser Lys Ala Trp Glu Phe Ala Asn Thr
420 425 430

Arg Lys Ser Tyr Trp Arg Ile Ala Asn Ser Pro Ile Leu Ser Thr Thr
435 440 445

Leu

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<212> PRT
<213> Pseudomonas alcaligenes

<220>
<221> PEPTIDE
<222> (1)..(449)

<400> 15

Met Pro Pro Val Gly Val Ala Val Ser Leu Val Thr Val Met Gln Lys
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Phe Pro Thr Ala Glu Thr Val Ile Pro Asn Pro Gly Gln Lys Pro Arg
20 25 30

Val Met Pro Asp Ser Ala Lys Val Pro Ala Ala Ser Ala Thr Trp Thr
35 40 45

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Asn Ala Glu Pro Asp Thr Leu Met Glu Arg Val Leu Ala Pro Ala Asn
50 55 60

Leu Arg Arg Ala Tyr Gln Arg Val Val Ser Asn Lys Gly Ala Pro Gly
65 70 75 80

Ala Asp Gly Met Thr Val Ala Asp Leu Ala Gly Tyr Val Lys Gln Tyr
85 90 95

Trp Pro Thr Leu Lys Ala Arg Leu Leu Ala Gly Glu Tyr His Pro Gln
100 105 110

Ala Val Arg Ala Val Glu Ile Pro Lys Pro Gln Gly Gly Thr Arg Gln
115 120 125

Leu Gly Ile Pro Ser Val Val Asp Arg Leu Ile Gln Gln Ala Leu Gln
130 135 140

Gln Gln Leu Thr Pro Ile Phe Asp Pro Leu Phe Ser Lys Tyr Ser Tyr
145 150 155 160

Gly Phe Arg Pro Gly Arg Ser Thr His Gln Ala Ile Glu Met Ala Arg
165 170 175

Ala His Val Thr Ala Gly His Arg Trp Cys Val Glu Leu Asp Leu Glu
180 185 190

Lys Phe Phe Asp Arg Val Asn His Asp Ile Leu Met Ala Cys Ile Glu
195 200 205

Arg Arg Ile Lys Asp Lys Cys Val Leu Arg Leu Ile Arg Arg Tyr Leu
210 215 220

Glu Ala Gly Ile Met Ser Gly Gly Val Val Ser Pro Arg Gln Glu Gly
225 230 235 240

Thr Pro Gln Gly Gly Pro Leu Ser Pro Leu Leu Ser Asn Ile Leu Leu
245 250 255

Asp Glu Leu Asp Arg Glu Leu Glu Arg Arg Gly His Arg Phe Val Arg
260 265 270

Tyr Ala Asp Asp Ala Asn Ile Tyr Val Arg Ser Pro Arg Ala Gly Glu
275 280 285

Arg Val Leu Val Ser Val Glu Arg Phe Leu Arg Glu Arg Leu Lys Leu
290 295 300

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Thr Val Asn Arg Lys Lys Ser Gln Val Ala Arg Ala Trp Lys Cys Asp
305 310 315 320

Tyr Leu Gly Tyr Gly Met Ser Trp His Gln Gln Pro Arg Leu Arg Val
325 330 335

Ala Arg Met Ser Leu Asp Arg Leu Arg Asp Arg Leu Arg Met Leu Leu
340 345 350

Arg Ser Val Arg Ala Arg Lys Met Ala Thr Val Ile Glu Arg Ile Asn
355 360 365

Pro Val Leu Arg Gly Trp Ala Ser Tyr Phe Lys Leu Ser Gln Ser Lys
370 375 380

Arg Pro Leu Glu Glu Leu Asp Gly Trp Val Arg His Lys Leu Arg Cys
385 390 395 400

Val Ile Trp Arg Gln Trp Lys Gln Pro Pro Thr Arg Leu Arg Asn Leu
405 410 415

Met Arg Leu Gly Leu Ser Glu Glu Arg Ala Asn Lys Ser Ala Phe Asn
420 425 430

Gly Arg Gly Pro Trp Trp Asn Ser Gly Ala Gln His Met Asn Tyr Ala
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Leu

<210> 16
<211> 1620
<212> DNA
<213> *Geobacillus stearothermophilus*

<220>
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gaaggagaag gagaagatca cgatggcttt gttggaacgc atcttagcga gagacaacct	180
catcacggcg ctcaaacggg tcgaagccaa ccaaggagca ccgggaatcg acggagtatc	240
aaccgatcaa ctccgtgatt acatccgcgc tcactggagc acgatccgcg cccaactctt	300

ggcgggaacc	taccggccgg	cgctgtccg	cagggtcggg	atccccgaaac	cgggcggcgg	360
cacacggcag	ctaggcattc	ccaccgtggt	ggaccggctg	atccaacaag	ccattcttca	420
agaactcaca	cccattttcg	atccagactt	ctcccccttc	agcttcggat	tccgtccggg	480
ccgtaacgcc	cacgatgccg	tgcggcaagc	gcaaggctac	atccaggaag	ggtatcggta	540
cgtggtcgac	atggacctgg	aaaagtctct	tgatcgggtc	aacctgaca	tcttgatgag	600
tcgggtggcc	cgaaaagtca	aggataaacg	cgtgctgaaa	ctgatccgtg	cctacctgca	660
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ccccctcagc	cccctgctgg	cgaacatcct	tctcgacgat	ttagacaagg	aattggagaa	780
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acagcggatt	cgacagctga	ccaacccaaa	ctggagcata	tcgatgccag	aacgaattca	1080
tcgcgtcaat	caatacgtca	tgggatggat	cgggtatttt	cggtcgtcg	aaaccccgtc	1140
tgtccttcag	accatcgaag	gatggattcg	gaggaggctt	cgactctgtc	aatggcttca	1200
atggaacagg	gtcagaacca	gaatccgtga	gttaagagcg	ctggggctga	aagagacagc	1260
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gccacgcgaa	acggccatga	acgtcaagcc	cttctccttg	ttagatcgtc	tccttcccgc	1560
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Partial DNA sequence of Tirt plasmid #16

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 <222> (4)..(7)
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<220>
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 <222> (11)..(11)
 <223> n is a, c, g, or t

<220>
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 <223> n is a, c, g, or t

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 <223> n is a, c, g, or t

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 ggcagcagcc atcatcatca tcatcacagc agcggcctgg tgccgcgcgg cagccatatg 180
 cggcaagacc tgaatctcat cccgcggaag gagaagatca cgatggcttt gtggaacgc 240
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<210> 18
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 <212> PRT
 <213> Artificial

<220>
 <223> Partial amino acid sequence generated from Tirt plasmid #16
 (pTirt#16)

<400> 18

Met Gly Ser Ser His His His His Ser Ser Gly Leu Val Pro
 1 5 10 15

Arg Gly Ser His Met Arg Gln Asp Leu Asn Leu Ile Pro Arg Lys Glu
 20 25 30

Lys Ile Thr Met Ala Leu Leu Glu Arg Ile Leu Ala Arg Asp Asn Leu
 35 40 45

Ile Thr Ala Leu Lys Arg Val Glu Ala Asn Gln Gly Ala
 50 55 60